

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 12:24:53 ; Search time 2190.82 Seconds

(without alignments)
13201.892 Million cell updates/sec

Title: US-10-019-214-1

Perfect score: 822
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 37577330 seqs, 17593059518 residues

Total number of hits satisfying chosen parameters: 75154660

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	772.6	94.0	819	US-10-218-381-2	Sequence 2, Appl1
4	754.8	91.8	822	US-08-761-066-185	Sequence 185, Appl1
5	754.8	91.8	822	US-08-993-002A-3963	Sequence 3963, Ap
6	754.8	91.8	822	US-10-335-977-3963	Sequence 3963, Ap
7	753.2	91.6	9382	US-08-621-425-478	Sequence 478, Ap
8	750.2	91.3	837	US-08-993-002A-3964	Sequence 3964, Ap
9	750.2	91.3	837	US-10-335-977-3964	Sequence 3964, Ap
10	263.2	32.0	285	US-08-487-032A-119	Sequence 119, Ap
11	263.2	32.0	285	US-08-487-032C-119	Sequence 119, Ap
12	263.2	32.0	285	US-08-561-469A-119	Sequence 119, Ap
13	263.2	32.0	285	US-08-993-002A-9621	Sequence 9621, Ap
14	263.2	32.0	285	US-10-335-977-9621	Sequence 9621, Ap
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16	224.4	27.3	846	US-10-335-977-2792	Sequence 2792, Ap
17	224.4	27.3	888	US-08-993-002A-2793	Sequence 2793, Ap
18	224.4	27.3	888	US-10-335-977-2793	Sequence 2793, Ap
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44	53.8	6.5	7703	US-08-621-425-26	Sequence 26, Appl1
45	47	5.7	17569	US-09-897-516-94	Sequence 94, Appl1

ALIGNMENTS

RESULT 1
US-10-019-214-1
Sequence 1, Application US/10019214
GENERAL INFORMATION:
APPLICANT: Logan, Susan M.
APPLICANT: Wakarchuk, Warren
APPLICANT: Conlan, Wayne
APPLICANT: Monteiro, Mario A.
APPLICANT: Altman, Eleonora
APPLICANT: Hirasaka, Koji
TITLE OF INVENTION: GLYCOSYLTRANSFERASES OF HELICOBACTER PYLORI AS A NEW
TITLE OF INVENTION: TARGET IN PREVENTION AND TREATMENT OF H. PYLORI
FILE REFERENCE: 12243.24USWO
CURRENT APPLICATION NUMBER: US/10/019.214
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: PCT/CA00/00777
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/140.820

PRIOR FILING DATE: 1999-06-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 822
TYPE: DNA
ORGANISM: Helicobacter pylori
US-10-019-214-1

Query Match 100.0%; Score 822; DB 43; Length 822;
Best Local Similarity 100.0%; Pred No. 1.2e-212;
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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Sequence 9, Application US/10019214

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; GENERAL INFORMATION:
; APPLICANT: Logan, Susan M.
; APPLICANT: Wakarchuk, Warren
; APPLICANT: Conlan, Wayne
; APPLICANT: Monteiro, Mario A.
; APPLICANT: Altman, Eleonora
; APPLICANT: Hirasaka, Koji
; TITLE OF INVENTION: GLYCOSYLTRANSFERASES OF HELICOBACTER PYLORI AS A NEW
; TITLE OF INVENTION: TARGET IN PREVENTION AND TREATMENT OF H. PYLORI
; TITLE OF INVENTION: INFECTIONS
; FILE REFERENCE: 1243.24USWO
; CURRENT APPLICATION NUMBER: US/10/019,214
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: PCT/CA00/00777
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/140,820
; PRIOR FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 822
; TYPE: DNA
; ORGANISM: Helicobacter pylori
; US-10-019-214-9

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Query Match 94.0%; Score 773; DB 43; Length 822;

Best Local Similarity 96.3%; Pred. No. 2, 6e-199; Indels 0; Gaps 0;

Matches 791; Conservative 0; Mismatches 30;

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RESULT 3

US-10-218-381-2

Sequence 2, Application US/10218381

GENERAL INFORMATION: US/10218381

APPLICANT: Satoshi KOIZUMI.

APPLICANT: Tetsuo ENDO

APPLICANT: Kazuhiko TABATA

APPLICANT: AKIO OZAKI

TITLE OF INVENTION: GLYCOSYLTRANSFERASE AND DNA ENCODING THE SAME

FILE REFERENCE: 2139.18

CURRENT APPLICATION NUMBER: US/10/218,381

PRIOR FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: US/09/601,519

PRIOR FILING DATE: 2000-08-02

PRIOR APPLICATION NUMBER: PCT/JP99/00321

PRIOR FILING DATE: 1999-01-27

PRIOR APPLICATION NUMBER: JP 10-023389

PRIOR FILING DATE: 1998-02-04

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 819

TYPE: DNA

ORGANISM: Helicobacter pylori

US-10-218-381-2

Query Match 94.0%; Score 772.6; DB 47; Length 819;

Best Local Similarity 96.5%; Pred. No. 3, 3e-199; Indels 0; Gaps 0;

Matches 790; Conservative 0; Mismatches 29;

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DB 421 TTAGAAAAACATCAAGATTAAGCTATATCCGTTATGATGATTTATGATAGCG 480

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DB 421 TTGAAAAACATCCAGAGTTAGCTATGTCCTGATGATATTAATGACCCC 480
 QY 481 AGTGTAAAAAGTGGCCATTTAGCCATAAACAAGATACAGAGCGTGGGATC 540
 DB 481 AATGTTAAAAAGTGGCCATTTAGCCATAAACAAGATACAGAGCGTGGGATC 540
 QY 541 ATTAAAGCTTATAGCAAGGGGTGGGATCTCAAGCTATGATCAAGCTTAAGTTGCC 600
 DB 541 ATTAAAGCTTATAGCTATGATGCGGTGGGAGCAAGGCTATGATCAAGCTTAAGTTGCC 600
 QY 601 AAAGTTTTTTGAAATGACGCGGAAAAATGGGTTGTCCTGATATGATTAATGACGCT 660
 DB 601 AAAGTTTTTTGAAATGACGCGGAAAAATGGGTTGTCCTGATATGATTAATGACGCT 660
 QY 661 ACTTTATCATGCGCGTGAAGAAATCTGTGTACAACTTTGTGATGCGCTGATGAG 720
 DB 661 ACTTTATCATGCGCGTGAAGAAATCTGTGTACAACTTTGTGATGCGCTGATGAG 720
 QY 721 CAATCTCTACGATAGCAGAAAGAAAGAACTTATAGCCCTAAATGCGCTTAATGAGA 780
 DB 721 CAATCTCTACGATAGCAGAAAGAAAGAACTTATAGCCCTAAATGCGCTTAATGAGA 780
 QY 781 GAATCCATTTTAAATATTTGAAATTTGGCAGTTTGA 819
 DB 781 GAATCCATTTTAAATATTTGAAATTTGGCAGTTTGA 819

RESULT 4
 US-08-761-066-185

Sequence 185, Application US/08761066
 GENERAL INFORMATION:
 APPLICANT: DOUGLAS SMITH ET AL
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
 TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI AND
 NUMBER OF SEQUENCES: 714
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, Suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-ROM ISO9660
 COMPUTER:
 OPERATING SYSTEM:
 SOFTWARE:
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08761,066
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: GTN-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)227-5941
 INFORMATION FOR SEQ ID NO: 185:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 822 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

ORIGINAL SOURCE:
 ORGANISM: Helicobacter pylori
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1...822
 US-08-761-066-185

Query Match 91.8%; Score 754.8; DB 11; Length 822;
 Best Local Similarity 94.9%; Pred. No. 2,3e-194;
 Matches 780; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 TTGCGTGTGTTTGGCATTTCTTAAATCAAAAAGTGGGATCATTTGGTTAGTTT 60
 DB 1 TTGCGTGTGTTTATCATTTCTTTAAATCAAAAAGTGGGATCATTTGGTTAGTTT 60
 QY 61 AGAGACACCAAACTTTACTCAATAGCATCAATGCCACCAACCAAGCAAAATTTT 120
 DB 61 AGAGACACCAAACTTTACTCAATATATCAAGCCACCAACCAAGCAAAATTTT 120
 QY 121 GATCGATTTATTTCAAACTTTTGAAGCGGGTTGCACTTATGTAAGAAAGCATTTA 180
 DB 121 GATCGATTTATTTCAAACTTTTGAAGCGGGTTGCACTTATGTAAGAAAGCATTTA 180
 QY 181 CACCTTATTTCAATGCAAAACATCAAGATGGGATTAACAACCAATCTCATGAT 240
 DB 181 CACCTTATTTCAATGCAAAACATCAAGATGGGATTAACAACCAATCTCATGAT 240
 QY 241 GAGGTTCTAAGTTTATTTACGCTTTAAATATACATGCGAAGTTTATGAGCTTGGGGAG 300
 DB 241 GAGGTTCTAAGTTTATTTACGCTTTAAATATACATGCGAAGTTTATGAGCTTGGGGAG 300
 QY 301 CTGGGCTGATGCGATCTATATCTTGTGGGAAAAATGCTATGAACTCAATGAAGC 360
 DB 301 CTGGGCTGATGCGATCTATATCTTGTGTGGGAAAAATGCTATGAACTCAATGAAGC 360
 QY 361 ATCTGTATTTTGAAGACATATACCTTGAAGAGATTTTAAAGAGGCTTGAATTT 420
 DB 361 ATCTGTATTTTGAAGACATATACCTTGAAGAGATTTTAAAGAGGCTTGAATTT 420
 QY 421 TTGAAAAACATCCAGAGTTAGCTATATGCGCTTGAATGATTAATGATGATGCC 480
 DB 421 TTGAAAAACATCCAGAGTTAGCTATATGCGCTTGAATGATTAATGATGATGCC 480
 QY 481 AGTGTAAAAAGTGGCCATTTAGCCATAAACAAGATACAGAGCGTGGGATC 540
 DB 481 AGTGTAAAAAGTGGCCATTTAGCCATAAACAAGATACAGAGCGTGGGATC 540
 QY 541 ATTAAAGCTTATAGCAAGGGGTGGGATCTCAAGCTATGATCAAGCTTAAGTTGCC 600
 DB 541 ATTAAAGCTTATAGCTATGATGCGGTGGGAGCAAGGCTATGATCAAGCTTAAGTTGCC 600
 QY 601 AAAGTTTTTTGAAATGACGCGGAAAAATGGGTTGTCCTGATATGATTAATGACGCT 660
 DB 601 AAAGTTTTTTGAAATGACGCGGAAAAATGGGTTGTCCTGATATGATTAATGACGCT 660
 QY 661 ACTTTATCATGCGCGTGAAGAAATCTGTGTACAACTTTGTGATGCGCTGATGAG 720
 DB 661 ACTTTATCATGCGCGTGAAGAAATCTGTGTACAACTTTGTGATGCGCTGATGAG 720
 QY 721 CAATCTCTACGATAGCAGAAAGAAAGAACTTATAGCCCTAAATGCGCTTAATGAGA 780
 DB 721 CAATCTCTACGATAGCAGAAAGAAAGAACTTATAGCCCTAAATGCGCTTAATGAGA 780
 QY 781 GAATCCATTTTAAATATTTGAAATTTGGCAGTTTGA 822
 DB 781 GAATCCATTTTAAATATTTGAAATTTGGCAGTTTGA 822

RESULT 5
 US-08-993-002A-3963

Sequence 3963, Application US/08993002A
 GENERAL INFORMATION:
 APPLICANT: DOUGLAS SMITH et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,002A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3963:
SEQUENCE CHARACTERISTICS:
LENGTH: 822 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: circular
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...822
US-08-993-002A-3963
Query Match 91.8%; Score 754.8; DB 13; Length 822;
Best Local Similarity 94.9%; Pred. No. 2.3e-194;
Matches 780; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 361 ATCTGATTTTGAAGACGATATTAACCTTGAAAGAGATTTTAAAGAGGCTTGATTTT 420
DB ATCTGATTTTGAAGACGATATTAACCTTGAAAGAGATTTTAAAGAGGCTTGATTTT 420
QY 421 TTGAAAAACACATCCAGAGTTAGGCTTATCCGCTTGAGCATTTATTTGATGATGCC 480
DB TTGAAAAACACATCCAGAGTTAGGCTTATCCGCTTGAGCATTTATTTGATGATGCC 480
QY 481 AGTGTAAAGTGAGCCATTGAGCCATTAACCAAGAGATACAAAGCGTGTGGGATC 540
DB AGTGTAAAGTGAGCCATTGAGCCATTAACCAAGAGATACAAAGCGTGTGGGATC 540
QY 541 ATTAAGCTTATAGGAAAGGCTGGGAACTCAAGGCTATGTGATCAAGCTTAAGATTGCC 600
DB ATTAAGCTTATAGGAAAGGCTGGGAAAGGCTTGTGATGATCAAGCTTAAGATTGCC 600
QY 601 AAAGTTTTTTGAAATGCAAGCCGAAATGGGTGTTCTGTGATGATCAAGATGAGCGCT 660
DB AAAGTTTTTTGAAATGCAAGCCGAAATGGGTGTTCTGTGATGATCAAGATGAGCGCT 660
QY 661 ACTTTATCCATGGGCTGAAATAATCTGGTTTACCACTTTGTGATGATGATGATG 720
DB ACTTTATCCATGGGCTGAAATAATCTGGTTTGTACCACTTTGTGATGATGATGATG 720
QY 721 CAAATCTGATGATGACGAAAGAGAACTTATAGCCCTTAATAGCTTAATGAGA 780
DB CAAATCTGATGATGACGAAAGAGAACTTATAGCCCTTAATAGCTTAATGAGA 780
QY 781 GAATCTCATTTTAAATATTTGAAATATGGCAGTTTGTATTA 822
DB GAATCTCATTTTAAATATTTGAAATATGGCAGTTTGTATTA 822

RESULT 5

US-10-335-977-3963
Sequence 3963, Application US/10335977
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3963:
SEQUENCE CHARACTERISTICS:
LENGTH: 822 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Helicobacter pylori
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (8) LOCATION 1..822
 SEQUENCE DESCRIPTION: SEQ ID NO: 3963:
 US-10-335-977-3963

Query Match 91.8%; Score 754.8; DB 49; Length 822;
 Best Local Similarity 94.9%; Pred. No. 2.3e-194;
 Matches 780; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

```

QY 1 TTGCGTGTGTTTGGCCATTTCTTTAAATCAAAAAGTGTGGATACATTTGGTTAGTTTTT 60
DB 1 TTGCGTGTGTTTATCATTTCTTTAAATCAAAAAGTGTGGATAAATTTGGTTGTTTTT 60
QY 61 AGAGACACCACAATTACTCAATAGCATCAATGCCACCCACCAACCAAGCGAAATTTT 120
DB 61 AGAGACACCACAATTACTCAATATATCAACGCCACCCACCAAGCGAAATTTT 120
QY 121 GATGGGATTTATCTTAAACCTTTGAAGCGGGTTCACCCCTTAGTGAAAAAGCATTTA 180
DB 121 GATGGGATTTATCCAGACTTTTGAAGCGGGTTCACCCCTTAGTTAAAAAGCATTTA 180
QY 181 CACCCCTATTTCATCAGCAAAACATCAAAAGCATGGGATTTACAACCATCTCATAGT 240
DB 181 CACCCCTATTTCATCAGCAAAATATCAAAAGCATGGGATTTGCAACCATCTCATAGT 240
QY 241 GAGGTTTCTAAGTTTATTTAGCCTTTAAATACATGCGAAGTTTATGAGTTGGGGAG 300
DB 241 GAGGTTTCTAAGTTTATTTAGCCTTTAAATACATGCGAATTTATGAGTTGGGGAG 300
QY 301 CTGGGGTGTATGCGAGTATTTCTGTTGGGAAAAATGATAGAACTCAATAGAACG 360
DB 301 CTGGGGTGTATGCGAGCATTTATTCGTTGGCAAAAATGATAGAGCTCAATAGAACG 360
QY 361 ATCTGTATTTAGAAAGCATATTAACCTTGAAAGAGATTTTAAAGAGGCTTGGATTT 420
DB 361 ATCTGTATTTAGAAAGCATATTAACCTTGAAAGAGATTTTAAAGAGGCTTGGATTT 420
QY 421 TTAGAAAAACATCCAGAGTTAGGCTATATCCGCTTGATGATTTATTTGATAGTGC 480
DB 421 TTAGAAAAACATCCAGAGTTAGGCTATATCCGCTTGATGATTTATTTGATAGTGC 480
QY 481 AGGTAAAAAGTGAAGCATTTGAGCATAAAAACAAGATCAAGAGCGTGTGGGATC 540
DB 481 AGCGTAAAAAGTGAAGCATTTTAAACATTAACCAAGATCAAGAGCGTGTGGGATC 540
QY 541 ATTTAAGCTTATAGCGAAAGGGGTGAGCTCAAGGCTATGTGATCAAGCTTAAGTTC 600
DB 541 ATTTAAGCTTATAGCGATGGGGTGGGAGCGCAAGGCTATGTGATCAAGCTTAAGTTC 600
QY 601 AAAGTTTTTTTAAACACAGCCGAAATGGGTGTTCCGTGAGATACGATTAATGACCT 660
DB 601 AAAGTTTTTTTAAACACAGCCGAAATGGGTGTTCCGTGAGATACGATTAATGACCT 660
QY 661 ACTTTATTCATGCGGTGAAAAATCTGTGTACACACTTTTGTGATCGCTGATGATGAG 720
DB 661 ACTTTATTCATGCGGTGAAAAATCTGTGTACACACTTTTGTGATCGCTGATGATGAG 720
QY 721 CAAATCTCTAGATAGCAGAAAGAAAGAACTTATAGCCCTTAAATGCGCTTAATGGA 780
DB 721 CAAATCTCTAGATAGCAGAAAGAAAGAAAGAACTTATAGCCCTTAAATGCGCTTAATGGA 780
QY 781 GAATCCATTTTAAATATTTGAATATTTGGCAGTTTGTATTA 822
DB 781 GAATCCATTTTAAATATTTGAATATTTGGCAGTTTGTATTA 822

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RESULT 7

US-08-621-425-478/C
 ; Sequence 478; Application US/08621425
 ; GENERAL INFORMATION:
 ; APPLICANT: Douglas Smith
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
 ; TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 ; NUMBER OF SEQUENCES: 495
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: LAHIVE & COCKFIELD
 ; STREET: 60 State Street, Suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 8mm cartridge tape
 ; COMPUTER: SPARC station LX
 ; OPERATING SYSTEM: sunos4
 ; SOFTWARE: tar
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/621,425
 ; FILING DATE: 25-MARCH-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/561,469
 ; FILING DATE: 17-NOV-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/487,032
 ; FILING DATE: 07-JUNE-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragouras, Amy E.
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: GTN-001CP2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)227-5941
 ; INFORMATION FOR SEQ ID NO: 478:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9382 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORGANISM: Helicobacter pylori
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1..9382
 ; US-08-621-425-478

Query Match 91.8%; Score 753.2; DB 10; Length 9382;
 Best Local Similarity 94.8%; Pred. No. 1.6e-193;
 Matches 779; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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QY 1 TTGCGTGTGTTTGGCCATTTCTTTAAATCAAAAAGTGTGGATACATTTGGTTAGTTTTT 60
DB 2757 TTGCGTGTGTTTATCATTTCTTTAAATCAAAAAGTGTGGATAAATTTGGTTGTTTTT 2698
QY 61 AGAGACACCACAATTACTCAATAGCATCAATGCCACCCACCAACCAAGCGAAATTTT 120
DB 2697 AGAGACACCACAATTACTCAATATATCAAGCGCAACCCACCAAGCGCAATTTT 2638
QY 121 GATGGGATTTATCTTAAACCTTTGAAGCGGGTTCACCCCTTAGTGAAAAAGCATTTA 180
DB 2637 GATGGGATTTATCTCAAGACTTTTGAAGCGGGTTCACCCCTTAGTTAAAAAGCATTTA 2578
QY 181 CACCCCTATTTCATCAGCAAAACATCAAAAGCATGGGATTTACAACCAATCTCATAGT 240
DB 2577 CACCCCTATTTCATCAGCAAAATATCAAAAGCATGGGATTTGCAACCATCTCATAGT 2518
QY 241 GAGGTTTCTAAGTTTATTTAGCCTTTAAATACATGCGAAGTTTATGAGCTTGGGGAG 300

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Db      2517 GAGGTTCTTAAGTTTATTATCGCTTAAATACCGAAATTTATGAGCTTGGGGAG 2458
Qy      301 CTTGGGTCATACCGAGTCTTATTCCTTGTGGAAAAATGCATACCATGAAAGG 360
Db      2457 CTTGGGTCATACCGAGTCTTATTCCTTGTGGAAAAATGCATACCATGAAAGG 2398
Qy      361 ATCTGATTTTAAAGACATATACCTTGAAGAGATTTTAAAGAGGCTTGATTTT 420
Db      2397 ATCTGATTTTAAAGACATATACCTTGAAGAGATTTTAAAGAGGCTTGATTTT 2338
Qy      421 TTAGAAAAACATCCAGAGTTAGGCTATATCCCTTGATGATTTATGATGCC 480
Db      2337 TTAGAAAAACATCCAGAGTTAGGCTATATCCCTTGATGATTTATGATGCC 2278
Qy      481 AGGTGTAAGTGAAGCATTGAGCCATTAACCAAGAGTAAAGAGGTGTGGGATC 540
Db      2277 AGGTGTAAGTGAAGCATTTAACCATGAACCAAGAGTAAAGAGGTGTGGGATC 2218
Qy      541 ATTAAGCTTATAGCGAAGGGGTGGGACTCAAGGCTATGATCAAGCCTAAGATTGCC 600
Db      2217 ATTAAGCTTATAGCGAAGGGGTGGGACTCAAGGCTATGATCAAGCCTAAGATTGCC 2158
Qy      601 AAAGTTTTTTTGAATGACACCGGAAAAATGGGTTGCTGTGATACGATATGACGCT 660
Db      2157 AAAGTTTTTTTGAATGACACCGGAAAAATGGGTTGCTGTGATACGATATGACGCT 2098
Qy      661 ACTTTATCATAGCGGTGGAATAATCTGCTTCAACCTTTGTGATCGTGATGATGAG 720
Db      2097 ACTTTATCATAGCGGTGGAATAATCTGCTTCAACCTTTGTGATCGTGATGATGAG 2038
Qy      721 CAATCTCTACGATAGCAGAAAGAAACCTTATAGCCTTAAATCCGCTTAATGAGA 780
Db      2037 CAATCTCTACGATAGCAGAAAGAAACCTTATAGCCTTAAATCCGCTTAATGAGA 1978
Qy      781 GAACTCCATTTTAAATATTTGAATATTTGGCAGTTGTATTA 822
Db      1977 GAACTCCATTTTAAATATTTTGAATATTTGGCAGTTGTATTA 1936

```

RESULT 8 US-08-993-002A-3964

; Sequence 3964, Application US/08993002A
; GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD

STREET: 28 State Street
CITY: Boston

STATE: Massachusetts
COUNTRY: USA

ZIP: 02109-1875
COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible

OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,002A

PILING DATE:
PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400

TELEPHONE: (617)227-7400

```

; TELEPHAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3964:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 837 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1...837
; US-08-993-002A-3964

Query Match      91.3%; Score 750.2; DB 13; Length 837;
Best Local Similarity 94.7%; Pred. No. 4,2e-193; Indels 0; Gaps 0;
Matches 776; Conservative 0; Mismatches 43;

Qy      1 TTGCGTGTGTTGCGATTTCCTTAATCAAAAGTGTGCGATACATTTGGTTAGTTT 60
Db      19 TTGCGTGTGTTTATCATTTCTTTAAATCAAAAGTGTGCGATTAATTTGGTTGTTT 78
Qy      61 AGAGACACCAACATTTACTCAATAGATCAATGCAATGCCACCAACCAAGCGCAATTTT 120
Db      79 AGAGACACCAACATTTACTCAATATATCAACGCGACCAACCAAGCGCAATTTT 138
Qy      121 GATGCGATTATCTTAAACCTTTGAAGCGGGTGGACCCCTTGTAGTAAAGATTTA 180
Db      139 GATGCGATTATTTCAAGACTTTTGAAGCGGGTGGACCCCTTGTAAAGATTTA 198
Qy      181 CACCTTATTTGATCAGCAAAACATCAAGACATGGGATTTCAACCAATCTCATCACT 240
Db      199 CACCTTATTTGATCAGCAAAATATCAAGACATGGGATTTCAACCAATCTCATCACT 258
Qy      241 GAGGTTTCTAGATTATTTACGCTTTAAATNCAATGCGAAGTTTATGAGCTTGGGAG 300
Db      259 GAGGTTTCTAGATTATTTACGCTTTAAATNCAATGCGAAGTTTATGAGCTTGGGAG 318
Qy      301 CTTGGGTGCTATGCGAGTCAATTTCTTGTGGGAAAAATGATAGAACTCAATGAGCG 360
Db      319 CTTGGGTGCTATGCGAGTCAATTTCTTGTGGGAAAAATGATAGAACTCAATGAGCG 378
Qy      361 ATCTGATTTTGAAGACATATTAACCTTGAAGAGATTTTAAAGAGGCTTGATTTT 420
Db      379 ATCTGATTTTGAAGACATATTAACCTTGAAGAGATTTTAAAGAGGCTTGATTTT 438
Qy      421 TTAGAAAAACATCCAGAGTTAGGCTATATCCCTTGATGATTTATGATGATGCC 480
Db      439 TTAGAAAAACATCCAGAGTTAGGCTATATCCCTTGATGATTTATGATGATGCC 498
Qy      481 AGGTGTAAGTGAAGCATTGAGCCATTAACCAAGAGTAAAGAGGTGTGGGATC 540
Db      499 AGGTGTAAGTGAAGCATTTAACCATGAACCAAGAGTAAAGAGGTGTGGGATC 558
Qy      541 ATTAAGCTTATAGCGAAGGGGTGGGACTCAAGGCTATGATCAAGCCTAAGATTGCC 600
Db      559 ATTAAGCTTATAGCGAAGGGGTGGGACTCAAGGCTATGATCAAGCCTAAGATTGCC 618
Qy      601 AAAGTTTTTTTGAATGACACCGGAAAAATGGGTTGCTGTGATACGATATGACGCT 660
Db      619 AAAGTTTTTTTGAATGACACCGGAAAAATGGGTTGCTGTGATACGATATGACGCT 678
Qy      661 ACTTTATCATAGCGGTGGAATAATCTGCTTCAACCTTTGTGATCGTGATGATGAG 720
Db      679 ACTTTATCATAGCGGTGGAATAATCTGCTTCAACCTTTGTGATCGTGATGATGAG 738
Qy      721 CAATCTCTACGATAGCAGAAAGAAACCTTATAGCCTTAAATGCGCTTAATGAGA 780
Db      739 CAATCTCTACGATAGCAGAAAGAAACCTTATAGCCTTAAATGCGCTTAATGAGA 798

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Qy 781 GAATCCATTAAATATTTGAATAATATGGCAGTTTGA 819
 Db 799 GAATCCATTAAATTTTGAATATGTCGAGTTTGA 837

RESULT 9 US-10-335-977-3964

Sequence 3964, Application US/10335977
 GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
 RELATING TO HELICOBACTER PYLORI FOR
 DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 10031

CORRESPONDENCE ADDRESS:

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: Windows NT 4.0

SOFTWARE: UNIX

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/335,977

FILING DATE: 30-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/993,002

FILING DATE: 17-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: GTN-018

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 3964:

SEQUENCE CHARACTERISTICS:

LENGTH: 837 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Helicobacter pylori

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1..837

SEQUENCE DESCRIPTION: SEQ ID NO: 3964:

US-10-335-977-3964

Query Match 91.3%; Score 750.2; DB 49; Length 837;
 Best Local Similarity 94.7%; Pred. No. 4,2e-193;
 Matches 776; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 1 TTGCGTGTGTTTGCATTTCTTTAAATCAAAAAGTGTGGATACATTTGGTTAGTTT 60
 Db 19 TTGCGTGTGTTTATCATTTCTTTAAATCAAAAAGTGTGGATACATTTGGTTAGTTT 78
 Qy 61 AGAGACCAACAATTACTCAATAGCATGACCAACCAACCAACCAACCAATTTT 120
 Db 79 AGAGACCAACAATTACTCAATATATCAACGCCACCAACCAACCAACCAATTTT 138
 Qy 121 GATGGATTATTTCTAAACTTTTGAAGCGGGTTGCAACCCCTTAGTGAAGAACATT 180
 Db 139 GATGGATTATTTCTAAAGCTTTTGAAGCGGGTTGCAACCCCTTAGTGAAGAACATT 198
 Qy 181 CACCTTATTTGATCAGCAAAACATCAAAAGATGGGATTACACCAATCTCATGCT 240

Db 199 CACCTTATTTGATCAGCAAAACATCAAAAGATGGGATTACACCAATCTCATGCT 258
 Qy 241 GAGGTTCTAGTTTATTAACGCTTTAAATACCATGCAAGTTTATGACTTGGGGAG 300
 Db 259 GAGGTTCTAGTTTATTAACGCTTTAAATACCATGCAAGTTTATGACTTGGGGAG 318
 Qy 301 CTGGGTCTATGCAATCAATATTCCTTGTGGAAAAATGATAGAACTCAATGAAGC 360
 Db 319 CTGGGTCTATGCAATCAATATTCCTTGTGGAAAAATGATAGAACTCAATGAAGC 378
 Qy 361 ATCTGATTTTGAAGCAATATACCTTGAAGAGATTTTAAAGGGCTTGAATTT 420
 Db 379 ATCTGATTTTGAAGCAATATACCTTGAAGAGATTTTAAAGGGCTTGAATTT 438
 Qy 421 TTAGAAAAACATCCAAAGATTAGGCTATATCCGCTTGAATTTATGATGATCC 480
 Db 439 TTAGAAAAACATCCAAAGATTAGGCTATATCCGCTTGAATTTATGATGATCC 498
 Qy 481 AGGTAAAAAGTAGCCATTGACCATTAACCAAGATACAGAGCCGTGGGATC 540
 Db 499 AGGTAAAAAGTAGCCATTGACCATTAACCAAGATACAGAGCCGTGGGATC 558
 Qy 541 ATTAAGCTTATAGCAAGGGGTGGGACTCAAGGCTATGATCAAGGCTATGATGCC 600
 Db 559 ATTAAGCTTATAGCAAGGGGTGGGACTCAAGGCTATGATCAAGGCTATGATGCC 618
 Qy 601 AAAGTTTTTTGAAGTATGCAAGCAAGAAATGGGTTCTCTGTGATAGATAATGACGCT 660
 Db 619 AAAGTTTTTTGAAGTATGCAAGCAAGAAATGGGTTCTCTGTGATAGATAATGACGCT 678
 Qy 661 ACTTTATCCATGCGGTGAAAAATCTGTGTTACAACCTTTGTGATCGCTGATGATGAG 720
 Db 679 ACTTTATCCATGCGGTGAAAAATCTGTGTTACAACCTTTGTGATCGCTGATGATGAG 728
 Qy 721 CAAATCTCTAGATAGCAAGCAAGAAAGAACTTATAGCCCTTAATTCGCTTAATGAG 780
 Db 739 CAAATCTCTAGATAGCAAGCAAGAAAGAACTTATAGCCCTTAATTCGCTTAATGAG 798
 Qy 781 GAATCCATTAAATATTTGAATAATATGGCAGTTTGA 819
 Db 799 GAATCCATTAAATTTTGAATATGTCGAGTTTGA 837

RESULT 10 US-08-487-032A-119

Sequence 119, Application US/08487032A

GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR

NUMBER OF SEQUENCES: 880

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHYE & COCKFIELD

STREET: 60 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,032A

FILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: GTN-001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...285
OTHER INFORMATION: /note="influenzae type B
11pooligosaccharide"
US-08-487-032A-119

Query Match 32.0%; Score 263.2; DB 8; Length 285;
Best Local Similarity 95.4%; Pred. No. 1.1e-60;
Matches 271; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 214 ATGGGATTACCAACCAATCTCATGAGGTTTCTAAGTTTATTACGCTTTAAATAC 273
DB 1 ATGGGATTGCAACCACTTCATCATGAGGTTTCTAAGTTTATTACGCTTTAAATAC 60
QY 274 CATCGAATTATGAGCTTGGGGAGCTTGGTCTATGCAATATTCTTGTGG 333
DB 61 CATCGAATTATGAGCTTGGGGAGCTTGGTCTATGCAATATTCTTGTGG 120
QY 334 GAAAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 393
DB 121 CAAAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 180
QY 394 GAGGATTTAAAGAGGCTTGGATTTTAAAGAAACACATCCAGAGTTAGGCTATATC 453
DB 181 GAGGATTTAAAGAGGCTTGGATTTTAAAGAAACACATCCAGAGTTAGGCTATATC 240
QY 454 CGCTGATGCAATTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 497
DB 241 CGTTGATGCAATTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 284

RESULT 11
US-08-487-032C-119
Sequence 119, Application US/08487032C
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBLACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 941
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE +ACY- COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release +ACM-1.0, Version +ACM-1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,032C
FILING DATE: 07-Jun-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-001

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc+AF8-feature
LOCATION: 1...285
OTHER INFORMATION: /note+AD0- +ACI-influenzae type B
11pooligosaccharide+ACI-
SEQUENCE DESCRIPTION: SEQ ID NO: 119:
US-08-487-032C-119

Query Match 32.0%; Score 263.2; DB 8; Length 285;
Best Local Similarity 95.4%; Pred. No. 1.1e-60;
Matches 271; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 214 ATGGGATTACCAACCAATCTCATGAGGTTTCTAAGTTTATTACGCTTTAAATAC 273
DB 1 ATGGGATTGCAACCACTTCATCATGAGGTTTCTAAGTTTATTACGCTTTAAATAC 60
QY 274 CATCGAATTATGAGCTTGGGGAGCTTGGTCTATGCAATATTCTTGTGG 333
DB 61 CATCGAATTATGAGCTTGGGGAGCTTGGTCTATGCAATATTCTTGTGG 120
QY 334 GAAAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 393
DB 121 CAAAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 180
QY 394 GAGGATTTAAAGAGGCTTGGATTTTAAAGAAACACATCCAGAGTTAGGCTATATC 453
DB 181 GAGGATTTAAAGAGGCTTGGATTTTAAAGAAACACATCCAGAGTTAGGCTATATC 240
QY 454 CGCTGATGCAATTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 497
DB 241 CGTTGATGCAATTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 284

RESULT 12
US-08-561-469A-119
Sequence 119, Application US/08561469A
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBLACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 994
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,469A
FILING DATE: 17-Nov-1995
PRIOR APPLICATION NUMBER: US 08/487,032

FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-001CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...285 /note="influenzae type B
OTHER INFORMATION: lipooligosaccharide"
US-08-561-469A-119

Query Match 32.0%; Score 263.2; DB 9; Length 285;
Best Local Similarity 95.4%; Pred. No. 1.1e-60;

Matches 271; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 214 ATGGGATTACAACCATCTCATGAGCTTCTAAGTTTATTATAGCTTTAAATATAC 273
DB 1 ATGGGATTGCAACCACTCTCATGAGCTTCTAAGTTTATTATAGCTTTAAATATAC 60
QY 274 CATCGGAATTATAGCTTGGGGAGCTTGGTCTATGCGATCATTTATTCCTTGTGG 333
DB 61 CATCGGAATTATAGCTTGGGGAGCTTGGTCTATGCGAGCATTTATTCCTTGTGG 120
QY 334 GAAAATGATGAACTCAATGAAGGATCTGATTTTGAAGAGATATTAACCTTGAAA 393
DB 121 CAAAATGATAGCTCATAGAGCATCTGATTTTGAAGAGATATTAACCTTGAAA 180
QY 394 GAGATTTTAAAGAGGCTTGATTTTGAAGAAACACATCAAGAGTTAGGCTATATC 453
DB 181 GAGATTTTAAAGAGGCTTGATTTTGAAGAAACACATCAAGAGTTAGGCTATATC 240
QY 454 CGCTTGATGATTTATTTGATATGATGCGAGTGAAGAGTGAAGCC 497
DB 241 CGTTGATGATTTATTTGATATGATGCGAGTGAAGAGTGAAGCC 284

RESULT 13
US-08-993-002A-9621
Sequence 9621, Application US/08993002A

GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/993,002A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 9621:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...285
US-08-993-002A-9621

Query Match 32.0%; Score 263.2; DB 13; Length 285;
Best Local Similarity 95.4%; Pred. No. 1.1e-60;

Matches 271; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 214 ATGGGATTACAACCATCTCATGAGCTTCTAAGTTTATTATAGCTTTAAATATAC 273
DB 1 ATGGGATTGCAACCACTCTCATGAGCTTCTAAGTTTATTATAGCTTTAAATATAC 60
QY 274 CATCGGAATTATAGCTTGGGGAGCTTGGTCTATGCGAGTCAATTTATTCCTTGTGG 333
DB 61 CATCGGAATTATAGCTTGGGGAGCTTGGTCTATGCGAGCATTTATTCCTTGTGG 120
QY 334 GAAAATGATGAACTCAATGAAGGATCTGATTTTGAAGAGATATTAACCTTGAAA 393
DB 121 CAAAATGATAGCTCATAGAGCATCTGATTTTGAAGAGATATTAACCTTGAAA 180
QY 394 GAGATTTTAAAGAGGCTTGATTTTGAAGAAACACATCAAGAGTTAGGCTATATC 453
DB 181 GAGATTTTAAAGAGGCTTGATTTTGAAGAAACACATCAAGAGTTAGGCTATATC 240
QY 454 CGCTTGATGATTTATTTGATATGATGCGAGTGAAGAGTGAAGCC 497
DB 241 CGTTGATGATTTATTTGATATGATGCGAGTGAAGAGTGAAGCC 284

RESULT 14
US-10-335-977-9621
Sequence 9621, Application US/10335977

GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0

SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)742-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 9621:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...285
SEQUENCE DESCRIPTION: SEQ ID NO: 9621:
US-10-335-977-9621

Query Match 32.0%; Score 263.2; DB 49; Length 285;
Best Local Similarity 95.4%; Pred. No. 1,1e-60;
Matches 271; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 214 ATGGGAGTTCACCAACCAATTCATCAGTGAAGTTTCTAAGTTTATTCGCTTTAAATAC 273
1 ATGGGAGTTCACCAACCAATTCATCAGTGAAGTTTCTAAGTTTATTCGCTTTAAATAC 60
DB 274 CATGCCAAGTTTATGAGCTTGGGGAGCTTGGGTCATGAGTCAATTCCTTGTG 333
61 CATGCCAAGTTTATGAGCTTGGGGAGCTTGGGTCATGAGTCAATTCCTTGTG 120
QY 334 GAAAAATGATAGTCAATCAATGAAGCATCTGATTTTGAAGAGCATATTAACCTTGAA 333
121 CAAAAATGATAGTCAATCAATGAAGCATCTGATTTTGAAGAGCATATTAACCTTGAA 180
DB 394 GAGGATTTTAAAGAGGCTTGATTTTGAAGAAACACATCCAGAGTTAGGCTATATC 453
181 GAGGATTTTAAAGAGGCTTGATTTTGAAGAAACACATCCAGAGTTAGGCTATATC 240
QY 454 CGCTTGATGATTTATGTATGATGCCAGTGTAAAAAGTGAGCC 497
241 CGTTGATGATTTATGTATGATGCCAGTGTAAAAAGTGAGCC 284
DB

RESULT 15

US-08-993-002A-2792
Sequence 2792, Application US/08993002A
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,002A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2792:
SEQUENCE CHARACTERISTICS:
LENGTH: 846 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...846
US-08-993-002A-2792

Query Match 27.3%; Score 224.4; DB 13; Length 846;
Best Local Similarity 59.5%; Pred. No. 6e-50;
Matches 450; Conservative 0; Mismatches 276; Indels 30; Gaps 3;
QY 2 TGGGTGTTTTCACATTTCTTTAAATCAAAAAGTGTGCATCATTTGGTTTATGTTTAA 61
2 TGGGTGTTTTCATTTTATTTCAATTTAGCCCAAACTGTAAATTTTCTTTAAAGAAA 61
DB 62 GAGACCAACCACTTACATAGATCAATGACCAACCAACCAAGCGCAATTTTG 121
62 CTCATTAACCCCTTTAGAGAGCTTAACTTCAAGGATCTCTTATGAATTTTG 121
QY 122 ATGCAATTAATCTTAAACCTTTTGAAGGCGGTGCACCCCTTAGTGAAGAAAGATTAC 181
122 ATGCAATTAATCTTAAACCTTTTGAAGGCGGTGCACCCCTTAGTGAAGAAAGATTAC 181
DB 182 ACCCTTAATTCACGCAAAACATCAAGATGGG--GATTACACCAATTCATCA 238
182 ACCCTTAATTCATGTTAAGTGAAGTTATGCTTTTGTAAATATAAAAACACCCCTT 241
QY 239 GTGAGTTTCTAAGTTTATTAAGCTTTAAATACATGCGAAGTTATGAGCTTGGGG 298
239 GTGAGTTTCTAAGTTTATTAAGCTTTAAATACATGCGAAGTTATGAGCTTGGGG 298
DB 242 GCGCGTTAAAAAATTTCTTTAGCGCTCAACCATTTGGGAAAGAGATGGGTTGGGG 301
242 GCGCGTTAAAAAATTTCTTTAGCGCTCAACCATTTGGGAAAGAGATGGGTTGGGG 301
QY 299 AGCTTGGTGTATGAGATCATTAATTCCTTGTGGGAAAAATGATAGTCAATCAATGAAG 358
299 AGCTTGGTGTATGAGATCATTAATTCCTTGTGGGAAAAATGATAGTCAATCAATGAAG 358
DB 302 AGCTTGGTGTATGAGATCATTAATTCCTTGTGGGAAAAATGATAGTCAATCAATGAAG 361
302 AGCTTGGTGTATGAGATCATTAATTCCTTGTGGGAAAAATGATAGTCAATCAATGAAG 361
QY 359 CGATCTGATTTTGAAGAGATATTAACCTTGAAGAGAGATTTTAAAGAGGCTTGAT 418
359 CGATCTGATTTTGAAGAGATATTAACCTTGAAGAGAGATTTTAAAGAGGCTTGAT 418
DB 362 CGATCTGATTTTGAAGAGATATTAACCTTGAAGAGATTTTAAAGAGGCTTGAT 421
362 CGATCTGATTTTGAAGAGATATTAACCTTGAAGAGATTTTAAAGAGGCTTGAT 421
QY 419 TTTTGAAGAAACACATCCAGAGTTAGGCTATGCGCTTGAATTTATTTATGATG 478
419 TTTTGAAGAAACACATCCAGAGTTAGGCTATGCGCTTGAATTTATTTATGATG 478
DB 422 TTGGCCGACGACATCAAGATTTAGGCTTATGCGCTTGAATTTATTTATGATG 481
422 TTGGCCGACGACATCAAGATTTAGGCTTATGCGCTTGAATTTATTTATGATG 481
QY 479 CCAAGTGTAAAAAGTGAAGCATTTGAGCCATTAACCAAGATATCAAGAGCGTGGGGA 538
479 CCAAGTGTAAAAAGTGAAGCATTTGAGCCATTAACCAAGATATCAAGAGCGTGGGGA 538
DB 482 TGGCTAAACAAAAGACTCCAGTTA-----AAGGGTTTCTC 517
482 TGGCTAAACAAAAGACTCCAGTTA-----AAGGGTTTCTC 517

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Qy 539 TCATTAAAGCTTATAGCGAAGGGGTGGGACTCAAGGCTATGTGATCAGCCTTAAGATTG 598
Db 518 AAATTTAAATTTTAAAGATGCGACTCAAGGGTATGTTTAGCCCAAAAGCCG 577
Qy 599 CCAAGCTTTTGGAAATGACG---CGAAATGGTTGTTCTGTGATAGATATG 655
Db 578 CGCAAAATTTATGAATACAGCGCGAAAGAAATGGGTATGCTATAGATTGGGTATGG 637
Qy 656 ACGTACTTTTATCCATGGCGTGAAATATCTGGTGTACACCTTTTGTGATCGCTGATG 715
Db 638 ATAGGATTTATGGCATGGGCTCAAAAATCTATGTGTAGAGAAATTTGGATCGCTTGGC 697
Qy 716 ATGAGCAATCTCTACGATAGCAGCAAAAGAAAGAAC 751
Db 698 ACGGATTAACGCTCAAAATTCCAACACAGAAAGAAC 733

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 Job time : 2193.82 secs